SEQUENCE LISTING

<110> Boyle, William J.

<120> Osteoprotegerin Binding Proteins and Receptors

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<140> A-451B
<141> 1998-03-30

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<151> 1997-06-23

<150> 08,842,842
<151> 1997-04-16

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<170> PatentIn Ver. 2.1

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tcgcggagca gggcgcccga actccgggcg ccgcgcc atg cgc cgg gcc agc cga  175
                                        Met Arg Arg Ala Ser Arg
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gac tac ggc aag tac ctg cgc agc tcg gag gag atg ggc agc ggc ccc   223
Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro
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ggc gtc cca cac gag ggt ccg ctg cac ccc gcg cct tct gca ccg gct   271
Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala
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ccg gcg ccg cca ccc gcc gcc tcc cgc tcc atg ttc ctg gcc ctc ctg   319
Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu
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Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His
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tgc ttt tat aga atc ctg aga ctc cat gaa aac gca ggt ttg cag gac   463
Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp
            90                  95                 100

tcg act ctg gag agt gaa gac aca cta cct gac tcc tgc agg agg atg   511
Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met
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aaa caa gcc ttt cag ggg gcc gtg cag aag gaa ctg caa cac att gtg   559
Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val
    120                 125                 130

ggg cca cag cgc ttc tca gga gct cca gct atg atg gaa ggc tca tgg   607
Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp
135                 140                 145                 150

ttg gat gtg gcc cag cga ggc aag cct gag gcc cag cca ttt gca cac   655
Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His
                155                 160                 165

ctc acc atc aat gct gcc agc atc cca tcg ggt tcc cat aaa gtc act   703
Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr
            170                 175                 180

ctg tcc tct tgg tac cac gat cga ggc tgg gcc aag atc tct aac atg   751
Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met
        185                 190                 195

acg tta agc aac gga aaa cta agg gtt aac caa gat ggc ttc tat tac   799
Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr
    200                 205                 210

ctg tac gcc aac att tgc ttt cgg cat cat gaa aca tcg gga agc gta   847
Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val
215                 220                 225                 230

cct aca gac tat ctt cag ctg atg gtg tat gtc gtt aaa acc agc atc   895
Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile
                235                 240                 245

aaa atc cca agt tct cat aac ctg atg aaa gga ggg agc acg aaa aac   943
Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn
            250                 255                 260

tgg tcg ggc aat tct gaa ttc cac ttt tat tcc ata aat gtt ggg gga   991
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly
        265                 270                 275

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Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe
295 300 305 310

aaa gtt cag gac ata gac tgagactcat ttcgtggaac attagcatgg 1135
Lys Val Gln Asp Ile Asp
315

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actaagagac atggcccacg gtgtatgaaa ctcacagccc tctctcttga gcctgtacag 1255

gttgtgtata tgtaaagtcc ataggtgatg ttagattcat ggtgattaca caacggtttt 1315

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tagagggccc tattctatag 2295

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50 55 60

Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
65 70 75 80

Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
85 90 95

Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
100 105 110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
115 120 125

Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
130 135 140

Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
145 150 155 160

Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
165 170 175

Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
180 185 190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
195 200 205

Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
225 230 235 240

Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
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Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
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cgcagacaag aaggggaggg agcgggagag ggaggagagc tccgaagcga gagggccgag 180

cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tcg 229
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1 5 10 15

gag gag atg ggc ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac 277
Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His
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gcc ccg ccg ccg cct gcg ccg cac cag ccc ccc gcc gcc tcc cgc tcc 325
Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser
35 40 45

atg ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc 373
Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
50 55 60

gtc gcc ctg ttc ttc tat ttc aga gcg cag atg gat cct aat aga ata 421
Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
65 70 75

tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa 469
Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu
80 85 90 95

aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta 517
Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu
100 105 110

ata cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg 565

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aaa gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag   661
Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys
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ctt gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc   709
Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile
160                 165                 170                 175

cca tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg   757
Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg
                180                 185                 190

ggt tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata   805
Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile
            195                 200                 205

gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga   853
Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg
        210                 215                 220

cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg   901
His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met
    225                 230                 235

gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg   949
Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu
240                 245                 250                 255

atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat   997
Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His
                260                 265                 270

ttt tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag   1045
Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu
            275                 280                 285

gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag   1093
Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
        290                 295                 300

gat gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat           1135
Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
    305                 310                 315

tgagccccag ttttttggagt gttatgtatt tcctggatgt ttggaaacat tttttaaaac 1195

aagccaagaa agatgtatat aggtgtgtga gactactaag aggcatggcc ccaacggtac 1255

acgactcagt atccatgctc ttgacctttgt agagaacacg cgtatttata gccagtggga 1315
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acagacatat ttaactggtg cactttgtaa attccctggg gaaaacttgc agctaaggag 1795

gggaaaaaaa tgttgtttcc taatatcaaa tgcagtatat ttcttcgttc tttttaagtt 1855

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Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
         35                  40                  45

Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
     50                  55                  60

Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
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Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
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130 135 140

Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
145 150 155 160

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
165 170 175

Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
180 185 190

Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
195 200 205

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
210 215 220

His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
225 230 235 240

Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
245 250 255

Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
260 265 270

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
275 280 285

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<210> 26
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20 25

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